



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/743,752A

DATE: 04/03/2003

TIME: 14:25:11

Input Set : A:\pf0559usn_seqlist.txt

Output Set: N:\CRF4\04032003\I743752A.raw

5 <110> APPLICANT: INCYTE PHARMACEUTICALS, INC.
6 BANDMAN, Olga
7 TANG, Y. Tom
8 CORLEY, Neil C.
9 AZIMZAI, Yalda
10 BAUGHN, Mariah R.
12 <120> TITLE OF INVENTION: HUMAN SCAD-RELATED MOLECULES, SCRM-1 AND SCRM-2
14 <130> FILE REFERENCE: PF-0559 USN
16 <140> CURRENT APPLICATION NUMBER: 09/743,752A
C--> 17 <141> CURRENT FILING DATE: 2003-02-11
19 <150> PRIOR APPLICATION NUMBER: PCT/US9916164
20 <151> PRIOR FILING DATE: 1999-07-16
22 <150> PRIOR APPLICATION NUMBER: US 09/116,750
23 <151> PRIOR FILING DATE: 1998-07-16
25 <150> PRIOR APPLICATION NUMBER: US 60/160,074
26 <151> PRIOR FILING DATE: 1998-07-16
28 <160> NUMBER OF SEQ ID NOS: 6
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33 <211> LENGTH: 278
34 <212> TYPE: PRT
35 <213> ORGANISM: HOMO SAPIENS
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <223> OTHER INFORMATION: Incyte Clone No: 1240869
41 <400> SEQUENCE: 1
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45 20 25 30
46 Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly Phe Ala Ile
47 35 40 45
48 Ala Arg Arg Leu Ala Gln Asp Arg Ala His Val Val Val Ser Ser Arg
49 50 55 60
50 Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr Leu Gln Gly Glu Gly
51 65 70 75 80
52 Leu Ser Val Thr Gly Thr Val Cys His Val Gly Lys Ala Glu Asp Arg
53 85 90 95
54 Glu Arg Leu Val Ala Thr Ala Val Lys Leu His Gly Gly Ile Asp Ile
55 100 105 110
56 Leu Val Ser Asn Ala Ala Val Asn Pro Phe Phe Gly Ser Ile Met Asp
57 115 120 125
58 Val Thr Glu Glu Val Trp Asp Lys Thr Leu Asp Ile Asn Val Lys Ala

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59 130 135 140
60 Pro Ala Leu Met Thr Lys Ala Val Val Pro Glu Met Glu Lys Arg Gly
61 145 150 155 160
62 Gly Gly Ser Val Val Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser
63 165 170 175
64 Pro Gly Phe Ser Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu
65 180 185 190
66 Asn Asn Thr Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn
67 195 200 205
68 Cys Leu Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp
69 210 215 220
70 Met Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
71 225 230 235 240
72 Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu Cys
73 245 250 255
74 Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val Gly Gly
75 260 265 270
76 Gly Thr Pro Ser Arg Leu
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79 <210> SEQ ID NO: 2
80 <211> LENGTH: 564
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84 <220> FEATURE:
85 <221> NAME/KEY: misc_feature
86 <223> OTHER INFORMATION: Incyte Clone No: 2060002
88 <400> SEQUENCE: 2
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90 1 5 10 15
91 Tyr Ala Tyr Pro Ser Asp Tyr Asp Met His Thr Gly Asp Pro Lys Gln
92 20 25 30
93 Asp Leu Ala Tyr Glu Arg Gln Tyr Glu Gln Gln Thr Tyr Gln Val Ile
94 35 40 45
95 Pro Glu Val Ile Lys Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser
96 50 55 60
97 Asp Leu Ile Asp Gln Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser
98 65 70 75 80
99 Ser Asp Val Ile Asp Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu
100 85 90 95
101 Asn Ser Trp Thr Lys Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp
102 100 105 110
103 Pro Glu Ala Glu Ala Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe
104 115 120 125
105 Leu Ile Leu Tyr Lys Glu Leu Tyr Tyr Arg His Ile Tyr Ala Lys Val
106 130 135 140
107 Ser Gly Gly Pro Ser Leu Glu Gln Arg Phe Glu Ser Tyr Tyr Asn Tyr
108 145 150 155 160
109 Cys Asn Leu Phe Asn Tyr Ile Leu Asn Ala Asp Gly Pro Ala Pro Leu
110 165 170 175

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 111 | Glu | Leu | Pro | Asn | Gln | Trp | Leu | Trp | Asp | Ile | Ile | Asp | Glu | Phe | Ile | Tyr |
| 112 | | | | 180 | | | | | 185 | | | | | | 190 | |
| 113 | Gln | Phe | Gln | Ser | Phe | Ser | Gln | Tyr | Arg | Cys | Lys | Thr | Ala | Lys | Lys | Ser |
| 114 | | | 195 | | | | | 200 | | | | | 205 | | | |
| 115 | Glu | Glu | Glu | Ile | Asp | Phe | Leu | Arg | Ser | Asn | Pro | Lys | Ile | Trp | Asn | Val |
| 116 | | 210 | | | | | 215 | | | | | 220 | | | | |
| 117 | His | Ser | Val | Leu | Asn | Val | Leu | His | Ser | Leu | Val | Asp | Lys | Ser | Asn | Ile |
| 118 | 225 | | | | 230 | | | | | | 235 | | | | | 240 |
| 119 | Asn | Arg | Gln | Leu | Glu | Val | Tyr | Thr | Ser | Gly | Gly | Asp | Pro | Glu | Ser | Val |
| 120 | | | | 245 | | | | | | 250 | | | | | 255 | |
| 121 | Ala | Gly | Glu | Tyr | Gly | Arg | His | Ser | Leu | Tyr | Lys | Met | Leu | Gly | Tyr | Phe |
| 122 | | | 260 | | | | | | 265 | | | | | | 270 | |
| 123 | Ser | Leu | Val | Gly | Leu | Leu | Arg | Leu | His | Ser | Leu | Leu | Gly | Asp | Tyr | Tyr |
| 124 | | | 275 | | | | | 280 | | | | | 285 | | | |
| 125 | Gln | Ala | Ile | Lys | Val | Leu | Glu | Asn | Ile | Glu | Leu | Asn | Lys | Lys | Ser | Met |
| 126 | | 290 | | | | | 295 | | | | | 300 | | | | |
| 127 | Tyr | Ser | Arg | Val | Pro | Glu | Cys | Gln | Val | Thr | Thr | Tyr | Tyr | Tyr | Val | Gly |
| 128 | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| 129 | Phe | Ala | Tyr | Leu | Met | Met | Arg | Arg | Tyr | Gln | Asp | Ala | Ile | Arg | Val | Phe |
| 130 | | | | 325 | | | | | | 330 | | | | | 335 | |
| 131 | Ala | Asn | Ile | Leu | Leu | Tyr | Ile | Gln | Arg | Thr | Lys | Ser | Met | Phe | Gln | Arg |
| 132 | | | | 340 | | | | | 345 | | | | | | 350 | |
| 133 | Thr | Thr | Tyr | Lys | Tyr | Glu | Met | Ile | Asn | Lys | Gln | Asn | Glu | Gln | Met | His |
| 134 | | | 355 | | | | 360 | | | | | | 365 | | | |
| 135 | Ala | Leu | Leu | Ala | Ile | Ala | Leu | Thr | Met | Tyr | Pro | Met | Arg | Ile | Asp | Glu |
| 136 | | 370 | | | | | 375 | | | | | 380 | | | | |
| 137 | Ser | Ile | His | Leu | Gln | Leu | Arg | Glu | Lys | Tyr | Gly | Asp | Lys | Met | Leu | Arg |
| 138 | 385 | | | | 390 | | | | | | 395 | | | | | 400 |
| 139 | Met | Gln | Lys | Gly | Asp | Pro | Gln | Val | Tyr | Glu | Glu | Leu | Phe | Ser | Tyr | Ser |
| 140 | | | | 405 | | | | | | 410 | | | | | 415 | |
| 141 | Cys | Pro | Lys | Phe | Leu | Ser | Pro | Val | Val | Pro | Asn | Tyr | Asp | Asn | Val | His |
| 142 | | | | 420 | | | | | 425 | | | | | 430 | | |
| 143 | Pro | Asn | Tyr | His | Lys | Glu | Pro | Phe | Leu | Gln | Gln | Leu | Lys | Val | Phe | Ser |
| 144 | | | 435 | | | | | 440 | | | | | 445 | | | |
| 145 | Asp | Glu | Val | Gln | Gln | Gln | Ala | Gln | Leu | Ser | Thr | Ile | Arg | Ser | Phe | Leu |
| 146 | | 450 | | | | | 455 | | | | | 460 | | | | |
| 147 | Lys | Leu | Tyr | Thr | Thr | Met | Pro | Val | Ala | Lys | Leu | Ala | Gly | Phe | Leu | Asp |
| 148 | 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| 149 | Leu | Thr | Glu | Gln | Glu | Phe | Arg | Ile | Gln | Leu | Leu | Val | Phe | Lys | His | Lys |
| 150 | | | | 485 | | | | | | 490 | | | | | 495 | |
| 151 | Met | Lys | Asn | Leu | Val | Trp | Thr | Ser | Gly | Ile | Ser | Ala | Leu | Asp | Gly | Glu |
| 152 | | | | 500 | | | | | 505 | | | | | 510 | | |
| 153 | Phe | Gln | Ser | Ala | Ser | Glu | Val | Asp | Phe | Tyr | Ile | Asp | Lys | Asp | Met | Ile |
| 154 | | | 515 | | | | | 520 | | | | | 525 | | | |
| 155 | His | Ile | Ala | Asp | Thr | Lys | Val | Ala | Arg | Arg | Tyr | Gly | Asp | Phe | Phe | Ile |
| 156 | | 530 | | | | | 535 | | | | | 540 | | | | |
| 157 | Arg | Gln | Ile | His | Lys | Phe | Glu | Glu | Leu | Asn | Arg | Thr | Leu | Lys | Lys | Met |
| 158 | 545 | | | | 550 | | | | | | 555 | | | | | 560 |
| 159 | Gly | Gln | Arg | Pro | | | | | | | | | | | | |

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162 <210> SEQ ID NO: 3
163 <211> LENGTH: 1280
164 <212> TYPE: DNA
165 <213> ORGANISM: HOMO SAPIENS
167 <220> FEATURE:
168 <221> NAME/KEY: misc_feature
169 <223> OTHER INFORMATION: Incyte Clone No: 1240869
172 <400> SEQUENCE: 3

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| 173 | gagtgaacc | cagacttgct | ggtctgatcc | atgcacatgg | ccaggctgct | aggcctctgt | 60 |
| 174 | gcctgggcac | ggaagtcggt | gcggatggcc | agctccagga | tgacccgccg | ggacccgctc | 120 |
| 175 | acaaataagg | tggccctggt | aacggcctcc | accgacggga | tcggcttcgc | catcgcccgg | 180 |
| 176 | cgttttgccc | aggacagggc | ccacgtggtc | gtcagcagcc | ggaagcagca | gaatgtggac | 240 |
| 177 | caggcggtg | ccacgctgca | gggggagggg | ctgagcgtga | cgggcaccgt | gtgccatgtg | 300 |
| 178 | gggaaggcgg | aggaccggga | gcggctggtg | gccacggctg | tgaagcttca | tggaggtatc | 360 |
| 179 | gatatacctag | tctccaatgc | tgctgtcaac | cctttctttg | gaagcataat | ggatgtcact | 420 |
| 180 | gaggaggtgt | gggacaagac | tctggacatt | aatgtgaagg | ccccagccct | gatgacaaag | 480 |
| 181 | gcagtgggtgc | cagaaatgga | gaaacgagga | ggcggctcag | tggtgatcgt | gtcttccata | 540 |
| 182 | gcagccttca | gtccatctcc | tggcttcagt | ccttacaatg | tcagtataaac | agccttgctg | 600 |
| 183 | ggcctcaaca | ataccctggc | catagagctg | gccccaaagg | acattagggt | gaactgccta | 660 |
| 184 | gcacctggac | ttatcaagac | tagcttcagc | aggatgctct | ggatggacaa | ggaaaaagag | 720 |
| 185 | gaaagcatga | aagaaaccct | gcggataaga | aggttaggcg | agccagagga | ttgtgctggc | 780 |
| 186 | atcgtgtctt | tcctgtgctc | tgaagatgcc | agctacatca | ctggggaaac | agtgggtggg | 840 |
| 187 | ggtggaggaa | ccccgtccc | cctctgagga | ccgggagaca | gccccacagg | cagagttggg | 900 |
| 188 | ctctagctcc | tggtgctggt | cctgcattca | cccactggcc | tttcccacct | ctgctcacct | 960 |
| 189 | tactgttcac | ctcatcaaat | cagttctgcc | ctgtgaaaag | atccagcctt | ccctgccgtc | 1020 |
| 190 | aagggtggcgt | cttactcggg | attcctgctg | ttgttgtggc | cttgggtaaa | ggcctcccct | 1080 |
| 191 | gagaacacag | gacaggcctg | ctgacaaggc | tgagtctacc | ttggcaaaga | ccaagatatt | 1140 |
| 192 | ttttcctggg | ccactgggga | atctgagggg | tgatgggaga | gaaggaaacct | ggagtggag | 1200 |
| 193 | gagcagagtt | gcaaattaac | aacttgcaaa | tgaggtgcaa | ataaaatgca | gatgattgcg | 1260 |
| 194 | cggttttgaa | aaaaaaaaaa | | | | | 1280 |

196 <210> SEQ ID NO: 4
197 <211> LENGTH: 1894
198 <212> TYPE: DNA
199 <213> ORGANISM: HOMO SAPIENS
201 <220> FEATURE:
202 <221> NAME/KEY: misc_feature
203 <223> OTHER INFORMATION: Incyte Clone No: 2060002
205 <400> SEQUENCE: 4

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| 206 | ctcgcaagcg | aggcagccat | gtcttatccc | gctgatgatt | atgagtctga | ggcggcttat | 60 |
| 207 | gacctctacg | cttatcccag | cgactatgat | atgcacacag | gagatccaaa | gcaggacctt | 120 |
| 208 | gcttatgaac | gtcagtatga | acagcaaacc | tatcagggtga | tccctgaggt | gatcaaaaac | 180 |
| 209 | ttcatccagt | atttccacaa | aactgtctca | gatttgattg | accagaaagt | gtatgagcta | 240 |
| 210 | caggccagtc | gtgtctccag | tgatgtcatt | gaccagaagg | tgtatgagat | ccaggacatc | 300 |
| 211 | tatgagaaca | gctggacca | gctgactgaa | agattcttca | agaatacacc | ttggcccag | 360 |
| 212 | gctgaagcca | ttgctccaca | ggttggaat | gatgctgtct | tcctgatttt | atacaaagaa | 420 |
| 213 | ttatactaca | ggcacatata | tgccaaagtc | agtgggggac | cttccttgga | gcagagggtt | 480 |
| 214 | gaatcctatt | acaactactg | caatctcttc | aactacattc | ttaatgccga | tggctctgct | 540 |
| 215 | ccccttgaa | tacccaacca | gtggctctgg | gatattatcg | atgagttcat | ctaccagttt | 600 |
| 216 | cagtcattca | gtcagtaccg | ctgtaagact | gccaaagagt | cagaggagga | gattgacttt | 660 |

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218 gtagacaaaat ccaacatcaa ccgacagttg gaggtataca caagcggagg tgaccctgag 780
219 agtgtggctg gggagtatgg gcggcactcc ctctacaaaa tgcttggtta cttcagcctg 840
220 gtcgggcttc tccgcctgca ctccctgtta ggagattact accaggccat caaggtgctg 900
221 gagaacatcg aactgaacaa gaagagtatg tattcccgtg tgccagagtg ccaggtcacc 960
222 acatactatt atgttgggtt tgcataattg atgatgcgtc gttaccagga tgccatccgg 1020
223 gtcttcgcca acatcctcct ctacatccag aggaccaaga gcatgttcca gaggaccacg 1080
224 tacaagtatg agatgattaa caagcagaat gagcagatgc atgcgctgct ggccattgcc 1140
225 ctcacgatgt accccatgcg tatcgatgag agcattcacc tccagctgcg ggagaaatat 1200
226 ggggacaaga tgttgcgcag gcagaaagg gacccacaag tctatgaaga acttttcagt 1260
227 tactcctgcc ccaagttcct gtcgcctgta gtgcccaact atgataatgt gcacccaac 1320
228 taccacaaag agcccttcct gcagcagctg aaggtgtttt ctgatgaagt acagcagcag 1380
229 gccagctttt caaccatccg cagcttcctg aagctctaca ccaccatgcc tgtggccaag 1440
230 ctggctggct tcctggacct cacagagcag gagttccgga tccagcttct tgtcttcaaa 1500
231 cacaagatga agaacctcgt gtggaccagc ggtatctcag ccctggatgg tgaatttcag 1560
232 tcagcctcag aggttgactt ctacattgat aaggacatga tccacatcgc ggacaccaag 1620
233 gtcgccaggc gttatgggga tttcttcac cgtcagatcc acaaatttga ggagcttaat 1680
234 cgaaccctga agaagatggg acagagacct tgatgatatt cacacacatt caggaacctg 1740
235 ttttgatgta ttataggcag gaagtgtttt tgctaccgtg aaacctttac ctatgcagc 1800
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237 aaaggatctt tggagccaga aaaaaaaaaa aaaa 1894
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239 <210> SEQ ID NO: 5

240 <211> LENGTH: 280

241 <212> TYPE: PRT

242 <213> ORGANISM: HOMO SAPIENS

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245 <221> NAME/KEY: misc_feature

246 <223> OTHER INFORMATION: GENBANK ID: g1079566

248 <400> SEQUENCE: 5

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252 20 25 30
253 Val Leu Ala Asn Arg Val Ala Val Val Thr Gly Ser Thr Ser Gly Ile
254 35 40 45
255 Gly Phe Ala Ile Ala Arg Arg Leu Ala Arg Asp Gly Ala His Val Val
256 50 55 60
257 Ile Ser Ser Arg Lys Gln Gln Asn Val Asp Arg Ala Met Ala Lys Leu
258 65 70 75 80
259 Gln Gly Glu Gly Leu Ser Val Ala Gly Ile Val Cys His Val Gly Lys
260 85 90 95
261 Ala Glu Asp Arg Glu Gln Leu Val Ala Lys Ala Leu Glu His Cys Gly
262 100 105 110
263 Gly Val Asp Phe Leu Val Cys Ser Ala Gly Val Asn Pro Leu Val Gly
264 115 120 125
265 Ser Thr Leu Gly Thr Ser Glu Gln Ile Trp Asp Lys Ile Leu Ser Val
266 130 135 140
267 Asn Val Lys Ser Pro Ala Leu Leu Leu Ser Gln Leu Leu Pro Tyr Met
268 145 150 155 160
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VERIFICATION SUMMARY

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date